F72 (SEQ ID NO: 6)	NFKKAAGGGGAKT	R 65-75
F9 (SEQ ID NO: 7)	QGSGQVNFKG	R 4-12
F9 (SEQ ID NO: 8)	NFKKAATPGGAAKT	R 65-75
F11 (SEQ ID NO: 9)	IPQGQGKVTFNG	R 4-15
F12 (SEQ ID NO: 10)	IPEGQGKVT	R 2-12
F1C (SEQ ID NO: 11)	NGGTVHFKGEVVN	R5-12
F1 (SEQ ID NO: 12)	TTVTVNGGTVHF	R4-15

Please delete the paragraph on page 10, lines 5-18, and replace it with the following paragraph:

Results indicated the following:

F serotype	Pilin A Sequence	Residue Positions	Homologous Protection
F71 (SEQ ID NO: 13)	PQGQGEVT	R 5-12	Yes
F71 (SEQ ID NO: 14)	PQGQGEVA	R 5-12	Yes
F71 (SEQ ID NO: 4)	NFKQLQGGAAKKG	R 65-77	Yes
F72 (SEQ ID NO: 5)	PQGQGKVT	R 5-12	Yes
F72 (SEQ ID NO: 6)	NFKKAAGGGGAKT	R 65-77	Yes
F9 (SEQ ID NO: 15)	TTVNGGTVH	R 4-12	Yes
F9 (SEQ ID NO: 8)	NFKKAATPGGAAKT	R 65-75	Yes
F11 (SEQ ID NO: 16)	IPQGQGKVTFNGTV	R 4-17	Yes
F12 (SEQ ID NO: 10)	IPEGQGKVT	R 4-12	Yes
F1C (SEQ ID NO: 11)	NGGTVHFKGEVVN	R 5-15	Yes
F1 (SEQ ID NO: 12)	TTVTVNGGTVHF	R4-15	Yes

Please delete the paragraph on page 10, lines 20-41, and replace it with the following paragraph:

One or a combination of pilin A vaccines comprising one or more of the following amino acid sequences that correspond to published and unpublished F pilin primary sequences would be protective against ascending, non-obstructive *Escherichia coli* urinary tract infections in anatomically normal women and males:

F serotype	Pilin A Sequence	Pilin A Residue Positions	Urinary Tract Protection Potential	New or Old Claim
F71 (SEQ ID NO: 13)	PQGQGEVT	R 5-12	Pyelonephritis	New
P71 (SEQ ID NO: 14)	PQGQGEVA	R 5-12	Pyelonephritis	New
F71 (SEQ ID NO: 4)	NFKQLQGGAAKKG	R65-77	Pyelonephritis	New
F72 (SEQ ID NO: 5)	PQGQGKVT	R 5-12	Pyelonephritis	New
F72 (SEQ ID NO: 6)	NFKKAAGGGGAKT	R65-77	Pyelonephritis	New
F9 (SEQ ID NO: 15)	TTVNGGTVH	R 4-12	Pyelonephritis	New
F9 (SEQ ID NO: 8)	NFKKAATPGGAAKT	R 65-75	Pyelonephritis	New
F11 (SEQ ID NO: 16)	IPQGQGKVTFNGTV	R 4-17	Pyelonephritis	New
F12 (SEQ ID NO: 10)	IPEGQGKVT	R 4-12	Pyelonephritis	New
F13 (SEQ ID NO: 1)	PQGQGKVT	R 5-12	Pyelonephritis	Old
F13 (SEQ ID NO: 17)	AKFGGMGAKKG	R 65-65	Pyelonephritis	Old
F1C (SEQ ID NO: 11)	NGGTVHFKGEVVN	R 5-15	Cystitis	New
F1 (SEQ ID NO: 12)	TTVTVNGGTVHF	R4-15	Cystitis	New

Please delete Table 2 on page 19 and replace it with the following Table:

TABLE 2. Primers used in this study

Primers	Oligonucleotide sequence	Description
T3	5' ATTAACCCTCACTAAAG 3' (SEQ ID NO: 18)	anneals to multiple cloning site of SK-
T7	5' AATACGACTCACTATAG 3' (SEQ ID NO: 19)	anneals to multiple cloning site of SK-
Reverse	5' AACAGCTATGACCATG 3' (SEQ ID NO: 20)	anneals to multiple cloning site of SK-
PGpHFD	5' ATGAGACTGCGATTCTCTGT 3' (SEQ ID NO: 21)	anneals to the TAC translational start region of all 4 *pap* H genes
PapHRE	5' TCCGTTTCTCACAATTCTGA 3' (SEQ ID NO: 22)	anneals to bp 509-528 of the *pap* H gene of pDAL201B, *pap*-21 and pHUR 849, *pap*-5 210bFD
5' CCTGAAATACGAGAATATTA 3' (SEQ ID NO: 23)		anneals 93-bp upstream of the TAC translational start region of the pap A gene of pHUR849, *pap*-5 (2)
210bRE	5' TAATATCTCGTATTTCAGG 3' (SEQ ID NO: 24)	the complement of 210bFD and anneals to the same 93-bp region as described for 210bF
FOR210b	5' TGGACTGGTATAACAATCGA 3' (SEQ ID NO: 25)	anneals 2.9 kb upstream of the TAC translational start region of the *pap* H gene of pDAL210B, pap-21
200aRE	5' TCCGTTTCGCACAATTCTGA 3' (SEQ ID NO: 26)	anneals to bp 511-528 of the *pap* H gene of pDAL2I OB, pap-17, and pap 200a, respectively
PapFOR[a]	5' AGTGGATTCATGCAGCATTTCT AGAAA 3' (SEQ ID NO: 27)	anneals to bp 258-270 of the *pap* A gene of pHUR849, *pap*-5 (2)
FORSEQ	5' TGGACCTCCTGAGCTA 3' (SEQ ID NO: 28)	anneals to bp 456-474 of the *pap* A gene of pHUR849, *pap*-5 (2)
PapREV[b]	5' GGGGCAGCCCTGCCGTCCCAA AT 3' (SEQ ID NO: 29)	anneals to bp 122-142 of the *pap* H gene of pHUR849, *pap*-5
REVSEQ	5' AAACACCATGAAACACACA 3' (SEQ ID NO: 30)	anneals to bp 41-61 of the *pap* H gene of pHUR849

[a] contains a single Bam HI restriction site single underlined.
[b] contains a single Sma I blunt end restriction site double underlined.

Please delete the paragraph on page 22, line 5 to page 23, line 6 and replace it with the following paragraph:

Nucleotide Sequences and Deduced *Pap*H Primary Structures

The plasmids pHUR849 (*pap*-5), pDAL201B (*pap*-21), pDAL210B (*pap*-17) and, pDAL200A (*pap*-200A), in *E coli* strain HB101 express digalactose-binding of the serotypes F13, $F7_1$, $F7_2$ and F9, respectively. The *pap* gene cluster responsible for regulation and biogenesis of these pili from *E. coli* strains J96, C1212 and, 3669 is 1U. diagrammed in FIG. 1. Sequence analysis of *pap*H genes from pDAL201B (*pap*-21), pDAL210B (*pap*-17) and, pDAL200A (*pap*-200A), was compared to the known nucleotide sequence of *pap*H gene of

pHUR849 (*pap*-5) (3). FIG. 2 shows a single 588-bp open reading frame with the same polarity as *pap*A (2, 4). Analyses of these *pap*H sequences revealed many typical features of prokaryotic gene organization. All four *pap*H gene sequences contained a potential ribosome-binding sites, ATG initiation codon signal sequence, and a TGA termination codon. A potential initiation codon ATG at position -22, preceded by a sequence corresponding to -AGGGT, which showed homology to ribosome-binding sites, was found 13-bp upstream in all four *pap*H sequences. A protein initiated here and ending at the TGA triplet at position 586 would encode a 195 amino acid polypeptide with a calculated molecular weight of 21.9 kd. The mature *Pap*H protein contains 173 amino acid residues. The NH_2-terminal amino acid sequence of the open reading frame has all the features of a signal peptide sequence. The deduced putative signal sequence for the *pap*H was located 22 codons upstream of their terminal Ala (FIG. 2). These sequences contained a highly hydrophobic region comprising an amino acids stretch of Ser-Val-Pro-Leu-Phe-Phe-Phe (residues -17 to -11 of SEQ ID NO: 32). There was a positively charge amino acid residue (Arg) at the position -21. The suggested cleavage sites between Ala -1 and gly +1 conforms to rules of prokaryotic signal cleavage sites and was similar to most other bacterial genes (12). In addition, the final *pap*H deletion derivatives, pKD849-5 (*pap*-5), pKD201B (*pap*-21), pKD210B-1 (*pap*-17) and pKD200A-8 (*pap*-200A), were also sequenced. In addition, sequencing into the *pap*A and *pap*C genes which flank the *pap*H gene (FIG. 1) of all four *pap*H deletion derivatives was carried out in order to insure that all three genes were in frame. Finally, the codon usage of the *pap*H genes of pDAL201B, pDAL210B and, pDAL200A, and *pap*H gene of pHUR849 were analyzed using a codon frequency computer program (13). The pattern of codon utilization was not significantly different among the genes.

In the Figures:

Please replace Figure 5 with replacement sheet Figure 5 submitted herewith to correct a typographical error in Figure 5B at position 58. Position 58 should recite a "Q" instead of an "O."

In the Claims:

1. (Presently Amended) An immunogenic composition comprising dissociated pili from a α-D-Galp-(1-4)-β-D-Galp (Gal-Gal) binding pilus-producing *Escherichia coli* bacteria, said pili comprising at least one immunogenic peptide inserted into the immunodominant region